AMENDMENT

Kindly amend the application, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows:

IN THE SPECIFICATION:

Please amend the specification as shown:

Page 11, lines 19-22, kindly rewrite the paragraph thereat to read as follows:

Figure 1A **(residues 62-227 of SEQ ID NO: 3 and residues 62-227 of SEQ ID NO: 9, respectively)** and 1B **(SEQ ID NO: 40 and residues 62-332 of SEQ ID NO: 9, respectively)** are diagrams showing the results of analysis of the human Conrad polypeptide ~~(SEQ ID NO: 3 and SEQ ID NO: 9 respectively)~~ using the HMM structural prediction software of pfam (http://www.sanger.ac.uk/Software/Pfam/search.shtml).

Page 20, lines 11-20, kindly rewrite the paragraph thereat to read as follows:

Conrad polypeptides are advantageously made by recombinant means, using known techniques. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. Such polypeptides may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis **(SEQ ID NO: 20)**, GAL4 (DNA binding and/or transcriptional activation domains) and β-galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences, such as a thrombin cleavage site. Preferably the fusion protein will not hinder the function of the protein of interest sequence.

Page 83, line 18, to page 84, line 5, kindly rewrite the paragraph thereat to read as follows:

In addition to the arm primer pairs (5'armF/5'armR and 3'armF/3'armR2), further primers specific to the CONRAD locus are designed for the following purposes: 5' and 3' probe primer pairs (5'prF/5'prR and 3'prF2/3'prR) to amplify two short 150-300bp fragments of non-repetitive genomic DNA external to and extending beyond each arm, to allow Southern analysis of the targeted locus, in isolated putative targeted clones; a mouse genotyping primer pair (hetF and hetR) which allows differentiation between wild-type, heterozygote and homozygous mice, when used in a multiplex PCR with a vector-specific primer, in this case, Asc306; and lastly, a target screening primer (5'scr) which anneals upstream of the end of the 5' arm region, and which produces a target event specific 1.8kb amplimer when paired with a primer specific to the 5' end of the vector (DR2). This amplimer can only be derived from template DNA from cells where the desired genomic alteration has occurred and allows the identification of correctly targeted cells from the background of clones containing randomly integrated copies of the vector. The location of these primers and the genomic structure of the CONRAD locus used in the targeting strategy is shown in SEQ ID NO: 18.

musConrad 5'prF DR2	CGAAATATGAAGGAGTAAGGAGAGCAG **(SEQ ID NO: 21)**
musConrad 5'prR	GATTGCGTTGACTTTGCATTAAATTCTG **(SEQ ID NO: 22)**
musConrad 5'scr DR2	CTACAGAATTTAATGCAAAGTCAACGCAATC **(SEQ ID NO: 23)**
musConrad 5'armF Not	tttgcggccgCAACATTTAAAATATATTCTGGGGCTG **(SEQ ID NO: 24)**
musConrad 5'armR Spe	aaaactagtGCGATGAATGAACTGTTCCCGAGTCAG **(SEQ ID NO: 25)**
musConrad 3'armF Asc	aaaggcgcgccAGACAGCGATTACGCGTGCACACTCAC **(SEQ ID NO: 26)**
musConrad 3'armR2 Fse	tttggccggcCTTTCCAGGCATCAATTGTTGCTGTTG **(SEQ ID NO: 27)**
musConrad 3'prF.2	GAAATTTGATCAGATTCACCCTTCATATCC **(SEQ ID NO: 28)**
musConrad 3'prR	AAGATTGTTATGTGCAGGCTGGAGGTG **(SEQ ID NO: 29)**

musConrad hetF	GGAGCACTCATTTTTGCCCTGGCGCTC	(SEQ ID NO: 30)
musConrad hetR a306	TCCGTGAGTGTGCACGCGTAATCGCTG	(SEQ ID NO: 31)
Asc306	AATGGCCGCTTTTCTGGATTCATCGAC	(SEQ ID NO: 32)
DR2	ATCATGGCCCTACCATGCGCTAAACAC	(SEQ ID NO: 33)

Page 86, lines 17-25, kindly rewrite the paragraph thereat to read as follows:

A polynucleotide having the sequence shown in SEQ ID NO: 13 (below) is obtained from the human CONRAD nucleic acid sequence (SEQ ID NO:7). The SEQ ID NO: 13 polynucleotide is amplified by PCR using the oligonucleotide primers ATGCAGGCGCTTAACATTACCCCG **(SEQ ID NO: 34)** and TGCCCACTGTCTAAAGGAGAATTC **(SEQ ID NO: 35)**. This is cloned into a pTOPO-Echo Donor vector module (Invitrogen pUniV5/His Cat# ET001-10). This is then recombined into a suitable expression vector according to the host/expression system to be used. Transfection of the resulting construct into a host strain and induction of expression (according to the manufacturer's instructions) yields a fusion protein having the sequence of SEQ ID NO: 14.

Page 87, lines 4-10, kindly rewrite the paragraph thereat to read as follows:

A polynucleotide having the sequence shown in SEQ ID NO: 15 is amplified by PCR using the oligonucleotide primers AAATAAAGCTTGCAATGCAGGCGCTTAACATTACC **(SEQ ID NO: 36)** and TATAAAGGATCCTTAATGCCCACTGTCTAAAGGAG **(SEQ ID NO: 37)** to incorporate new restriction sites, HinDIII and BamHI at the 5-prime and 3-prime ends respectively of Conrad. This is then digested and ligated into similarly digested pcDNA5-JE (Invitrogen Cat# - K6010-01 vector modified to remove BGH Poly-A).

Page 87, lines 14-21, kindly rewrite the paragraph thereat to read as follows:

A polynucleotide having the sequence shown in SEQ ID NO: 16 is amplified by PCR using the oligonucleotide primers AAATAAAGCTTGCAATGCAGGCGCTTAACATTACC **(SEQ ID NO: 38)** and TATAAAGGATCCTTACTTATCGTCGTCATCCTTGTAATCATGCCCACTGTCTAAAGGA G **(SEQ ID NO: 39)** to incorporate new restriction sites, HinDIII and BamHI at the 5-prime and 3-prime ends respectively of Conrad and to include a 3' fusion FLAG tag. This is then digested and ligated into similarly digested pcDNA5-JE (Invitrogen Cat# - K6010-01 vector modified to remove BGH Poly-A).

Kindly replace the previously filed sequence listing with the enclosed papers entitled --sequence listing--.